



# Full wwPDB X-ray Structure Validation Report ⓘ

May 2, 2016 – 01:59 PM EDT

PDB ID : 5HE2  
Title : Bovine GRK2 in complex with Gbetagamma subunits and CCG224406  
Authors : Cato, M.C.; Waninger-Saroni, J.; Tesmer, J.J.G.  
Deposited on : 2016-01-05  
Resolution : 2.79 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027457  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

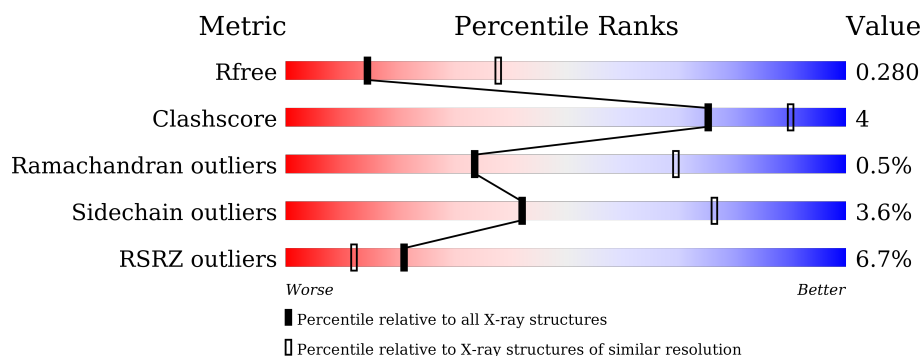
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	641	<div> <div>8%</div> <div>83%</div> <div>15%</div> <div>.</div> </div>
2	B	339	<div> <div>3%</div> <div>89%</div> <div>11%</div> <div>.</div> </div>
3	G	71	<div> <div>8%</div> <div>77%</div> <div>18%</div> <div>.</div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8290 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-adrenergic receptor kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	628	Total	C	N	O	S	0	1	0
			5155	3290	893	935	37			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	670	ALA	SER	engineered mutation	UNP P21146

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	339	Total	C	N	O	S	0	2	0
			2619	1613	470	513	23			

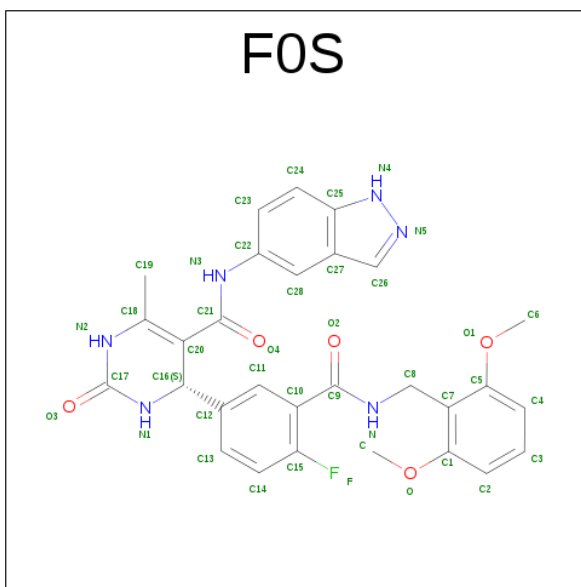
- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	58	Total	C	N	O	S	0	0	0
			444	277	79	85	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	68	SER	CYS	engineered mutation	UNP P59768

- Molecule 4 is (4 {S})-4-[3-[(2,6-dimethoxyphenyl)methylcarbamoyl]-4-fluoranyl-phenyl]- {N }-(1 {H}-indazol-5-yl)-6-methyl-2-oxidanylidene-3,4-dihydro-1 {H}-pyrimidine-5-carboxamide (three-letter code: F0S) (formula: C<sub>29</sub>H<sub>27</sub>FN<sub>6</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			41	29	1	6	5		

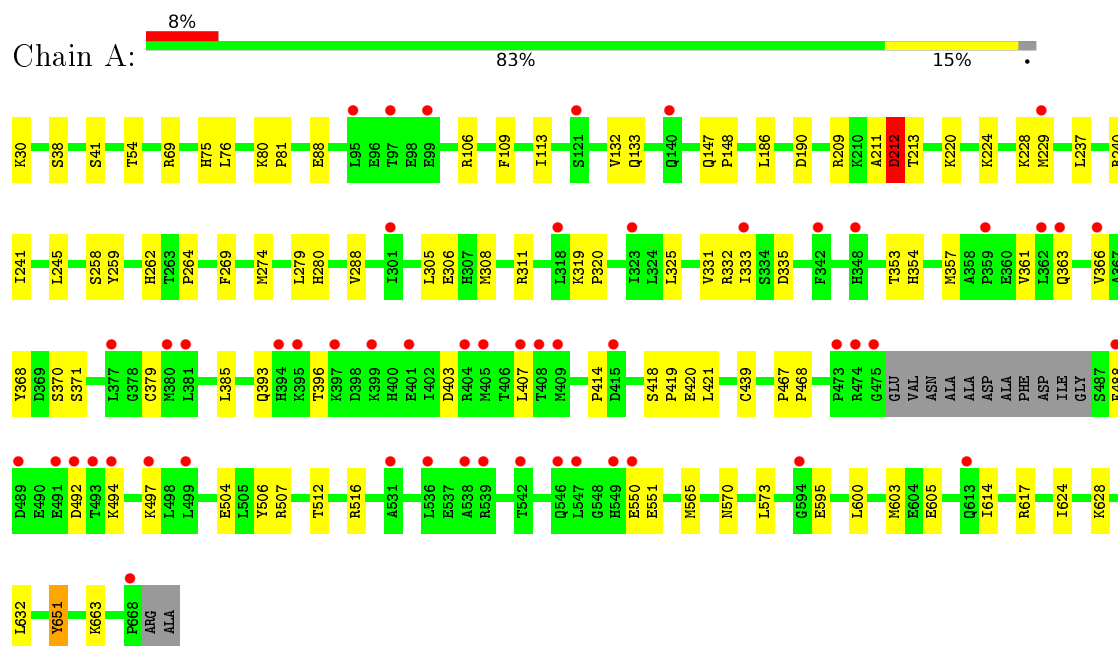
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	19	Total	O	0	0
			19	19		
5	B	12	Total	O	0	0
			12	12		

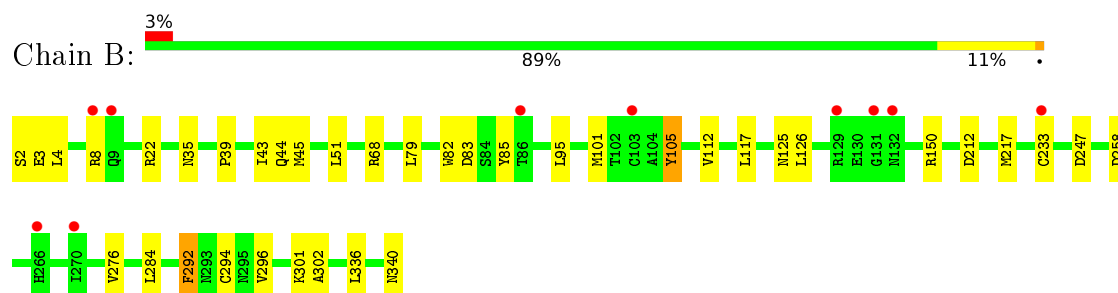
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

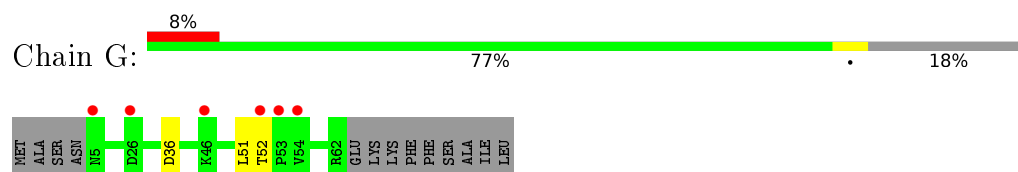
#### • Molecule 1: Beta-adrenergic receptor kinase 1



#### • Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



#### • Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.73Å 241.95Å 213.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.79 29.75 – 2.79	Depositor EDS
% Data completeness (in resolution range)	93.3 (30.00-2.79) 93.5 (29.75-2.79)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 2.80Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.198 , 0.277 0.205 , 0.280	Depositor DCC
$R_{free}$ test set	1883 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	61.5	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 32.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8290	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: F0S

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.59	0/5275	0.77	0/7089
2	B	0.60	0/2666	0.82	3/3613 (0.1%)
3	G	0.57	0/450	0.71	0/608
All	All	0.59	0/8391	0.78	3/11310 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	150	ARG	NE-CZ-NH1	6.29	123.45	120.30
2	B	212	ASP	CB-CG-OD1	5.48	123.23	118.30
2	B	247	ASP	CB-CG-OD1	5.09	122.88	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5155	0	5148	44	0
2	B	2619	0	2518	18	0
3	G	444	0	454	1	0
4	A	41	0	0	0	0
5	A	19	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	12	0	0	0	0
All	All	8290	0	8120	63	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (63) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:VAL:HA	1:A:368:TYR:CE2	2.31	0.66
1:A:212:ASP:HB3	1:A:213:THR:HG23	1.81	0.62
1:A:600:LEU:C	1:A:600:LEU:HD12	2.20	0.60
1:A:245:LEU:O	1:A:311:ARG:HD3	2.04	0.58
2:B:79:LEU:HG	2:B:95:LEU:HD21	1.88	0.55
1:A:614:ILE:O	1:A:617:ARG:HB3	2.06	0.55
1:A:605:GLU:HB3	1:A:624:ILE:HG23	1.89	0.55
1:A:565:MET:HE1	1:A:632:LEU:HD13	1.90	0.53
2:B:233[B]:CYS:SG	2:B:276:VAL:HG23	2.49	0.52
2:B:101:MET:HE1	2:B:117:LEU:HD23	1.90	0.52
1:A:279:LEU:HB2	1:A:320:PRO:O	2.10	0.52
1:A:229:MET:SD	1:A:494:LYS:HG3	2.51	0.51
2:B:105:TYR:HA	2:B:112:VAL:HG12	1.94	0.50
1:A:617:ARG:NE	1:A:617:ARG:HA	2.27	0.50
1:A:80:LYS:HB3	1:A:81:PRO:HD3	1.92	0.50
1:A:504:GLU:OE2	1:A:507:ARG:HD3	2.12	0.49
1:A:403:ASP:O	1:A:407:LEU:HD13	2.12	0.49
1:A:353:THR:O	1:A:357:MET:HG3	2.13	0.48
1:A:663:LYS:HG3	1:A:663:LYS:O	2.12	0.48
2:B:101:MET:CE	2:B:117:LEU:HD23	2.43	0.48
2:B:301:LYS:O	2:B:302:ALA:HB3	2.13	0.48
2:B:68:ARG:NE	2:B:85:TYR:CD2	2.81	0.48
1:A:418:SER:HB2	1:A:419:PRO:HD2	1.96	0.48
1:A:366:VAL:HA	5:A:806:HOH:O	2.14	0.47
1:A:258:SER:HA	1:A:516:ARG:HG3	1.95	0.47
1:A:186:LEU:HA	1:A:190:ASP:OD2	2.15	0.47
1:A:603:MET:HB3	1:A:651:TYR:HA	1.96	0.46
1:A:319:LYS:HG3	1:A:320:PRO:HD2	1.97	0.46
1:A:220:LYS:HB3	1:A:269:PHE:HB2	1.97	0.46
1:A:570:ASN:HB2	1:A:573:LEU:HB2	1.97	0.46
2:B:51:LEU:HB2	2:B:336:LEU:HB2	1.96	0.46
2:B:51:LEU:HB3	2:B:82:TRP:CE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:83:ASP:OD1	2:B:83:ASP:C	2.54	0.46
1:A:147:GLN:N	1:A:148:PRO:CD	2.78	0.46
1:A:354:HIS:HA	1:A:357:MET:HE2	1.98	0.46
1:A:393:GLN:O	1:A:396:THR:HG22	2.18	0.44
1:A:109:PHE:CE1	1:A:113:ILE:HG21	2.53	0.43
1:A:363:GLN:O	1:A:366:VAL:HB	2.18	0.43
2:B:4:LEU:O	2:B:8:ARG:HG3	2.18	0.43
1:A:550:GLU:O	1:A:551:GLU:C	2.56	0.42
2:B:284:LEU:HD13	2:B:296:VAL:HG11	2.02	0.42
2:B:51:LEU:HB3	2:B:82:TRP:CZ3	2.55	0.42
1:A:132:VAL:O	1:A:133:GLN:C	2.58	0.42
1:A:224:LYS:HE2	1:A:506:TYR:CD2	2.55	0.42
1:A:237:LEU:O	1:A:241:ILE:HD12	2.19	0.42
1:A:308:MET:HE1	1:A:333:ILE:HG21	2.00	0.42
1:A:30:LYS:HE3	1:A:211:ALA:HB3	2.02	0.42
2:B:45:MET:HA	2:B:340:ASN:O	2.19	0.42
1:A:259:TYR:CD1	1:A:512:THR:HG23	2.55	0.42
1:A:274:MET:SD	1:A:332:ARG:HD2	2.60	0.41
1:A:325:LEU:HG	1:A:331:VAL:HG12	2.03	0.41
1:A:288:VAL:HB	1:A:385:LEU:O	2.21	0.41
3:G:51:LEU:HD12	3:G:51:LEU:HA	1.89	0.41
1:A:420:GLU:HG2	1:A:421:LEU:H	1.86	0.41
2:B:292:PHE:CD1	2:B:292:PHE:N	2.88	0.41
2:B:22:ARG:NE	2:B:258:ASP:O	2.54	0.40
2:B:43:ILE:HG22	2:B:45:MET:HG3	2.02	0.40
1:A:305:LEU:O	1:A:306:GLU:C	2.59	0.40
2:B:125:ASN:OD1	2:B:126:LEU:N	2.54	0.40
1:A:325:LEU:N	1:A:325:LEU:HD12	2.37	0.40
1:A:467:PRO:HA	1:A:468:PRO:HD3	1.90	0.40
1:A:228:LYS:NZ	1:A:497:LYS:O	2.55	0.40
1:A:570:ASN:CB	1:A:573:LEU:HB2	2.51	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	625/641 (98%)	560 (90%)	61 (10%)	4 (1%)	30	65
2	B	339/339 (100%)	317 (94%)	21 (6%)	1 (0%)	46	79
3	G	56/71 (79%)	54 (96%)	2 (4%)	0	100	100
All	All	1020/1051 (97%)	931 (91%)	84 (8%)	5 (0%)	34	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	ASP
2	B	39	PRO
1	A	370	SER
1	A	414	PRO
1	A	264	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	567/574 (99%)	545 (96%)	22 (4%)	39	74
2	B	284/282 (101%)	276 (97%)	8 (3%)	51	84
3	G	47/58 (81%)	45 (96%)	2 (4%)	35	70
All	All	898/914 (98%)	866 (96%)	32 (4%)	42	76

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	SER
1	A	41	SER
1	A	54	THR
1	A	69	ARG
1	A	75	HIS

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Mol	Chain	Res	Type
1	A	76	LEU
1	A	88	GLU
1	A	106	ARG
1	A	209	ARG
1	A	212	ASP
1	A	240	ARG
1	A	262	HIS
1	A	280	HIS
1	A	335	ASP
1	A	371	SER
1	A	379	CYS
1	A	439	CYS
1	A	488	PHE
1	A	492	ASP
1	A	595	GLU
1	A	628	LYS
1	A	651	TYR
2	B	2	SER
2	B	3	GLU
2	B	35	ASN
2	B	44	GLN
2	B	105	TYR
2	B	217	MET
2	B	292	PHE
2	B	294	CYS
3	G	36	ASP
3	G	52	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	310	ASN
1	A	508	ASN
1	A	598	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	F0S	A	701	-	43,45,45	1.18	5 (11%)	55,64,64	2.49	20 (36%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	F0S	A	701	-	-	0/25/41/41	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	701	F0S	C16-C20	-2.84	1.49	1.51
4	A	701	F0S	C22-N3	-2.12	1.37	1.41
4	A	701	F0S	C18-N2	-2.06	1.34	1.38
4	A	701	F0S	C16-N1	2.01	1.48	1.47
4	A	701	F0S	C18-C20	2.95	1.47	1.36

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	F0S	O4-C21-C20	-5.05	112.47	121.17
4	A	701	F0S	C19-C18-C20	-4.06	121.39	127.67
4	A	701	F0S	O1-C5-C4	-3.75	118.05	124.35
4	A	701	F0S	O-C1-C2	-3.55	118.39	124.35
4	A	701	F0S	C21-C20-C18	-2.84	117.27	123.03
4	A	701	F0S	C14-C15-C10	-2.82	120.05	123.16
4	A	701	F0S	C15-C10-C9	-2.73	118.67	125.05
4	A	701	F0S	O2-C9-C10	-2.47	116.09	120.94
4	A	701	F0S	C23-C22-C28	-2.00	116.60	119.59
4	A	701	F0S	C-O-C1	2.17	120.70	117.53
4	A	701	F0S	C6-O1-C5	2.39	121.01	117.53
4	A	701	F0S	C11-C10-C15	2.60	119.15	116.83
4	A	701	F0S	C5-C7-C1	2.67	120.20	116.94
4	A	701	F0S	C19-C18-N2	3.06	119.10	113.39
4	A	701	F0S	C10-C9-N	3.74	125.19	117.52
4	A	701	F0S	C24-C25-N4	4.02	136.91	130.23
4	A	701	F0S	C20-C16-N1	4.11	112.23	109.09
4	A	701	F0S	N2-C17-N1	4.96	121.93	116.23
4	A	701	F0S	O1-C5-C7	6.70	121.84	115.44
4	A	701	F0S	O-C1-C7	6.83	121.97	115.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	628/641 (97%)	0.26	53 (8%) 14 6	39, 72, 127, 182	0
2	B	339/339 (100%)	0.04	10 (2%) 55 43	39, 56, 88, 145	0
3	G	58/71 (81%)	0.47	6 (10%) 9 4	46, 67, 112, 137	0
All	All	1025/1051 (97%)	0.20	69 (6%) 21 12	39, 64, 120, 182	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	408	THR	6.8
3	G	52	THR	6.8
1	A	409	MET	6.0
1	A	475	GLY	5.1
1	A	394	HIS	4.8
1	A	140	GLN	4.8
1	A	362	LEU	4.7
1	A	549	HIS	4.7
1	A	415	ASP	4.0
2	B	8	ARG	3.7
1	A	404	ARG	3.7
1	A	359	PRO	3.7
2	B	132	ASN	3.5
1	A	342	PHE	3.5
1	A	395	LYS	3.4
1	A	301	ILE	3.4
1	A	494	LYS	3.3
1	A	401	GLU	3.3
1	A	668	PRO	3.3
2	B	266	HIS	3.1
1	A	333	ILE	3.1
1	A	546	GLN	3.1
1	A	399	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	363	GLN	3.0
1	A	536	LEU	3.0
1	A	613	GLN	3.0
1	A	95	LEU	3.0
1	A	499	LEU	3.0
1	A	229	MET	2.9
1	A	547	LEU	2.9
1	A	489	ASP	2.9
1	A	377	LEU	2.9
3	G	53	PRO	2.9
1	A	497	LYS	2.9
1	A	348	HIS	2.9
1	A	474	ARG	2.7
1	A	405	MET	2.7
2	B	131	GLY	2.7
1	A	121	SER	2.7
1	A	488	PHE	2.6
1	A	407	LEU	2.6
3	G	46	LYS	2.5
2	B	233[A]	CYS	2.5
1	A	323	ILE	2.5
2	B	86	THR	2.5
1	A	492	ASP	2.5
1	A	99	GLU	2.5
1	A	550	GLU	2.5
2	B	129	ARG	2.5
1	A	493	THR	2.4
3	G	5	ASN	2.4
1	A	380	MET	2.4
1	A	318	LEU	2.4
1	A	491	GLU	2.3
1	A	473	PRO	2.3
1	A	539	ARG	2.3
2	B	270	ILE	2.3
2	B	9	GLN	2.3
3	G	54	VAL	2.3
1	A	366	VAL	2.2
1	A	538	ALA	2.2
1	A	542	THR	2.2
1	A	397	LYS	2.1
1	A	381	LEU	2.1
1	A	594	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
3	G	26	ASP	2.1
1	A	97	THR	2.1
2	B	103	CYS	2.1
1	A	531	ALA	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	F0S	A	701	41/41	0.95	0.19	0.15	43,62,68,82	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.